



Figure 1







GENE	RT-PCR ES EB	ES/EB	ES (\pm SE)	NORMALIZED ABUNDANCE IN GERM CELLS	MOUSE ORTHOLOGUES	MOTIFS
Hs.2860		154	1228 \pm 107	76%	Pou1f1/Oct4	homeobox
Hs.67624		519	1096 \pm 30	78%	-	nuclear localization and leucine zipper domains
Hs.351262		55	625 \pm 187	95%	-	-
Hs.86154		31	1319 \pm 81	66%	Tex17	'cold-shock' DNA-binding and zinc finger domains
Hs.189095		27	665 \pm 51	58%	-	C2H2 zinc finger domains
GPDH						

Figure 2

Summary:

The Affymetrix probeset 231381_at. exhibited an ES/EB ratio of 385. This probeset was derived from the Human UniGene cluster Hs.67624. This cluster is composed of 24 individual EST sequences most of which are derived from ES cell lines and germ cell tumors. It is also represented by the Genbank sequence BF223023. This mRNA appears to be encoded within the intron of another gene, the voltage-gated calcium channel alpha(2)delta-3 subunit gene. This mRNA appears to be transcribed from an endogenous human retrovirus which has been spliced to a non-viral sequence at its 3' end. This 3' sequence is unique in the genome. This mRNA does not appear to encode a complete protein. The 3' exon of the mRNA shares similarity with the Rat low density lipoprotein receptor-related protein 2 however this exon contains stop codons suggesting that it may represent a transcript derived from a pseudogene.

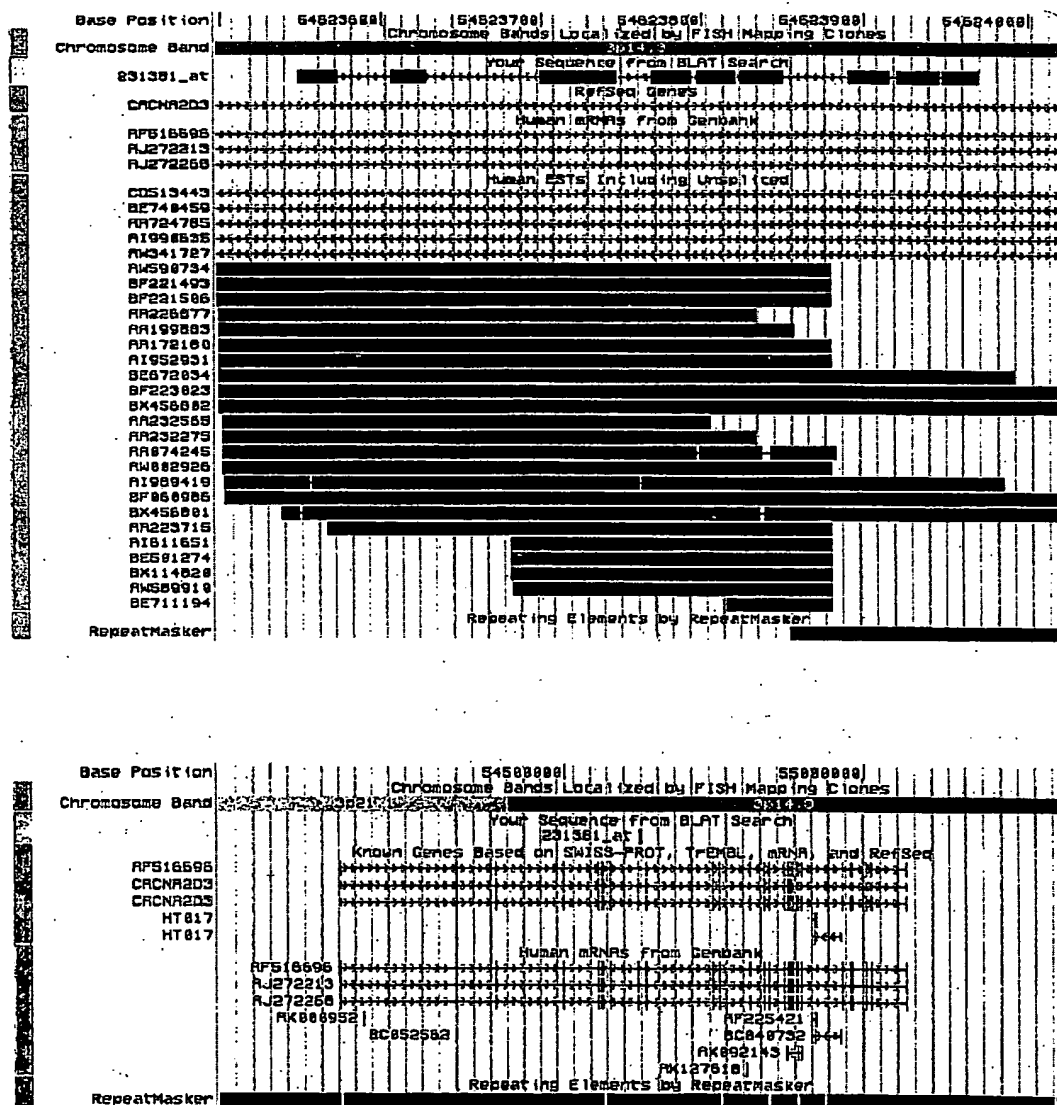
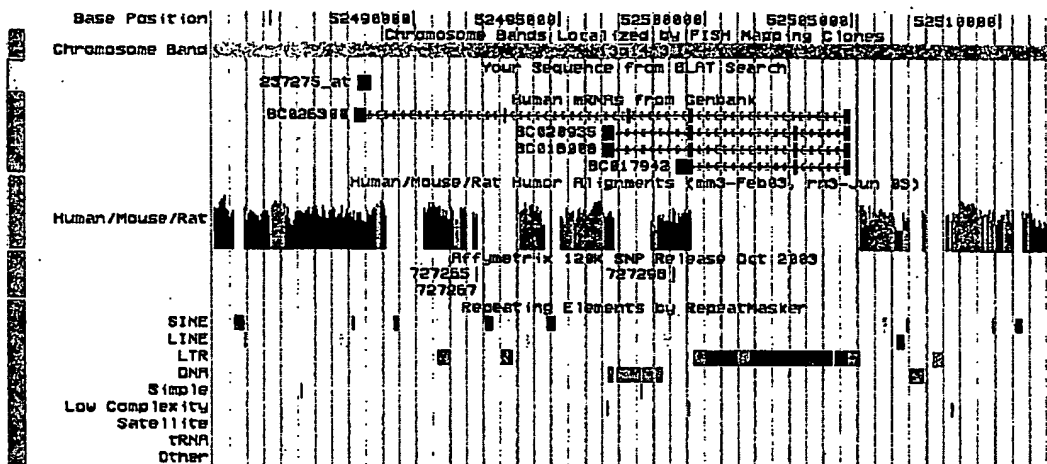


Figure 3

The Affymetrix probeset 237275_at exhibited an ES/EB ratio of 39. This probeset was derived from the Human Unigene cluster Hs.143925 which is also represented by the Genbank clone BC026300. This mRNA is composed of five exons and is encoded by a gene located on Chromosome 13. This gene appears to encode three different related mRNAs represented by BC026300, BC018008 and BC017942 as displayed below, but the 237275_at probeset is specific for the 3' exon of BC026300.



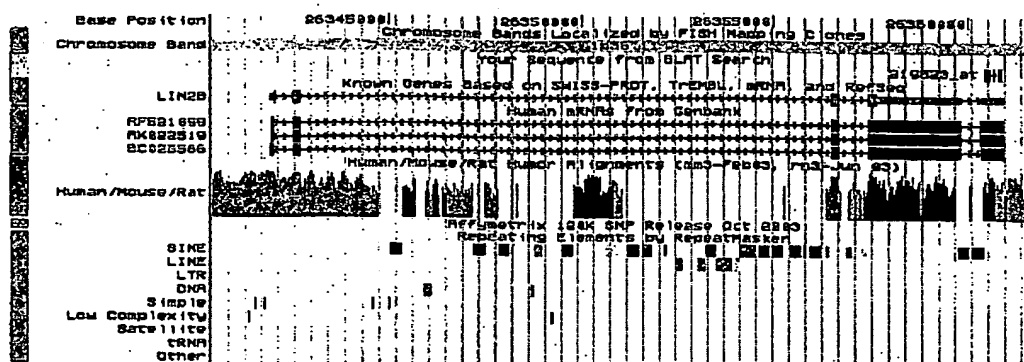
The BC026300 mRNA has three exons that contain repetitive DNA sequences and two exons that contains unique DNA sequences that have been conserved across the mouse, rat and human genomes.

Protein:

The longest open reading within this mRNA is located in the 3' exon containing unique sequences. The amino acid sequence of this open reading frame does not appear to be similar to any known protein. Comparison of this peptide to the Pfam database <http://pfam.wustl.edu/> using hmmssearch reveals no similarity to known protein motifs. Analysis of this coding sequence with the methods of Fickett (NAR 10(17); 5303-5318 (1982)) and Gribskov et al. (NAR 12(1); 539-549 (1984)) as implemented in The GCG Wisconsin Package applications Testcode and CodonPreference suggest that this sequence may not actually encode protein.

Figure 4

The Affymetrix probeset 219823_at exhibited an ES/EB ratio of 26. This probeset was derived from the Human Unigene cluster Hs.86154 which is also represented by the RefSeq clone NM_024674. This mRNA encodes a 209 amino acid protein (below) that is similar to the *c. elegans* lin-28 RNA-binding protein.



Protein Motifs:

Comparison of the protein derived from this sequence to the Pfam database <http://pfam.wustl.edu/> using hmmsearch reveals the presence of a Cold-shock DNA-binding domain sequence and Zinc knuckle domain sequence as diagrammed below. The presence of these sequences suggest that this protein is involved in binding RNA or single stranded DNA.



Hydropathy:

Kyte-Doolittle Hydropathy Plot (window size = 9)

A hydropathy plot of this protein indicates that is a relatively hydrophilic protein with no transmembrane domains (see below).

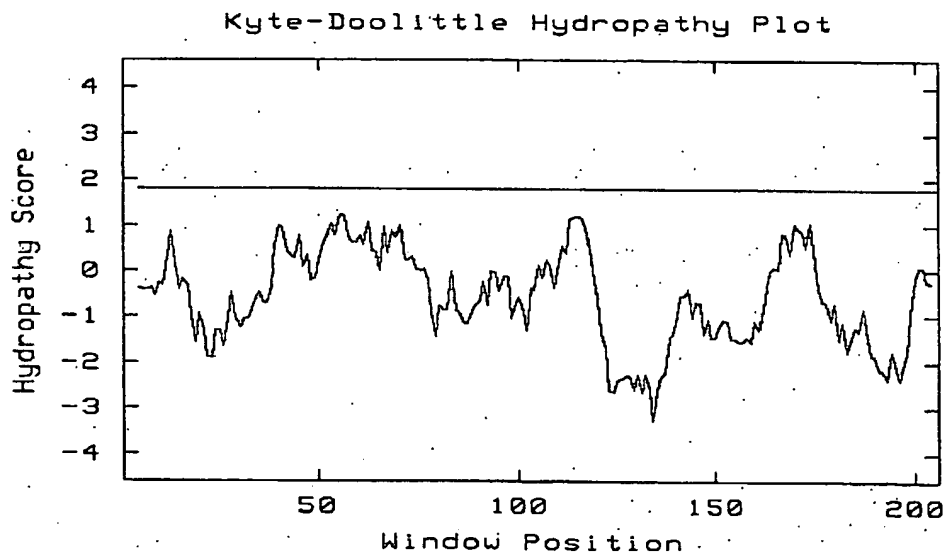
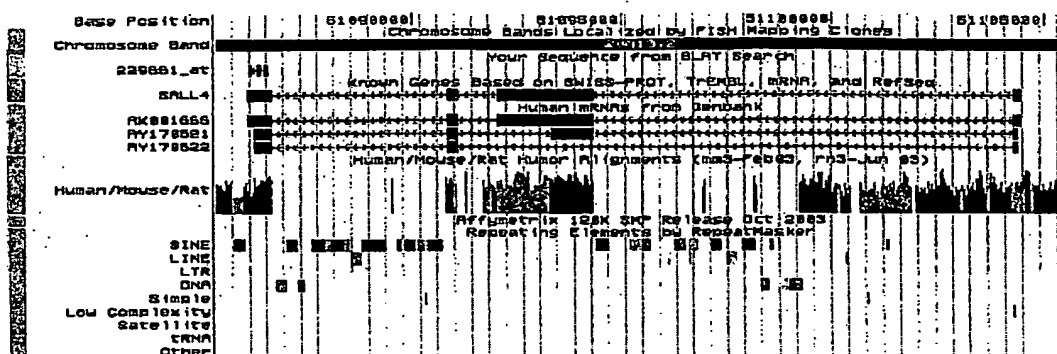


Figure 5

The Affymetrix probeset 229661_at exhibited an ES/EB ratio of 23. This probeset was derived from the Human Unigene cluster Hs.189095 which is also represented by the RefSeq clone NM_020436. This mRNA is encoded by a gene located on Chromosome 20 that has been genetically linked to the congenital ophthalmoplegia 'Duane radial ray syndrome'. This mRNA encodes a 1053 amino acid protein known as Sall4 that is a member of a family of proteins that contain a C2H2 zinc finger domain and are thought to be transcription factors.



Protein Motifs:

Comparison of the protein derived from this sequence to the Pfam database

<http://pfam.wustl.edu/> using hmmsearch reveals the presence of seven C2H2 zinc finger domains as diagrammed:



Hydropathy:

Kyte-Doolittle Hydropathy Plot (window size = 9)

A hydropathy plot of this protein indicates that is a relatively hydrophilic protein with no transmembrane domains (see below).

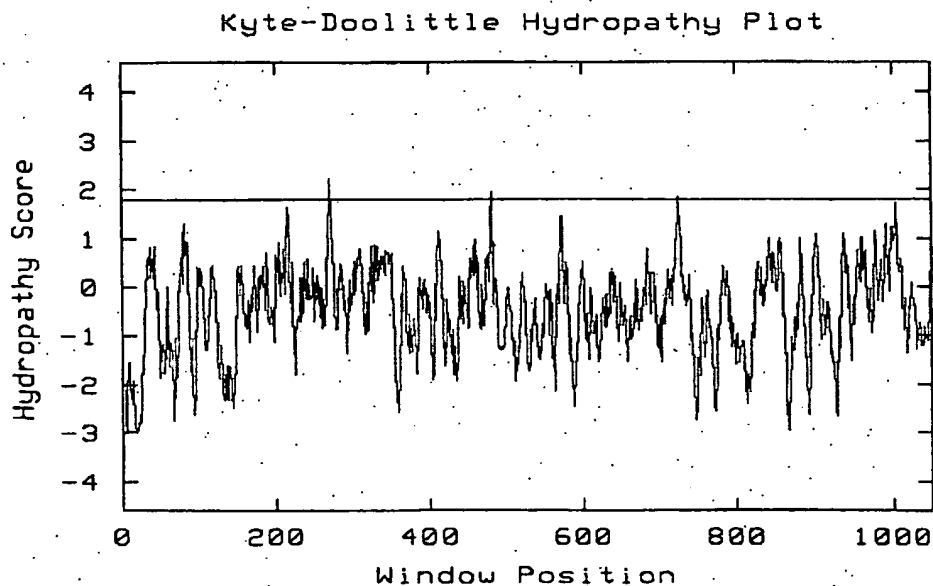
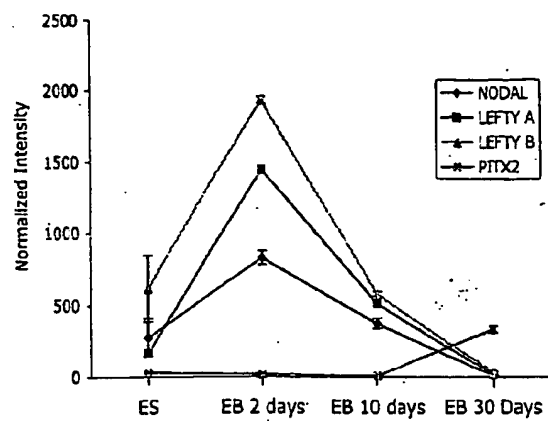


Figure 6

A



B

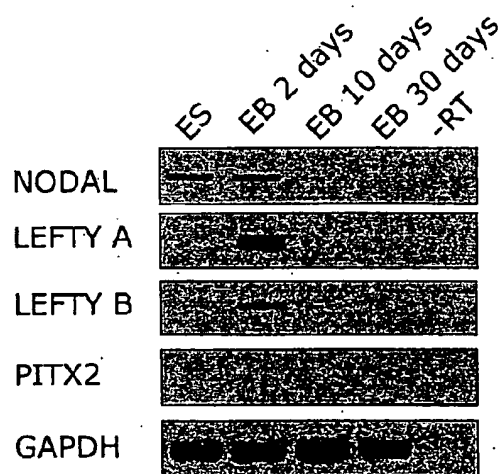


Figure 7

No.	ES/EB	Probe Set Name	Title	Unigene	Genbank
1	755 216405_at		gene encoding beta-galactoside-binding lectin	Hs.287389	M14087.1
2	385 231381_at		??? chr 3 , small prot. No similarity, multiple ESTs	<u>Hs.67624</u>	BF223023
3	243 208286_x_at		POU domain, class 5, transcription factor 1	Hs.2860	NM_002701.1
4	166 224344_at		cytochrome C oxidase subunit VIa homolog		AF020589.1
5	156 223642_at		Zic family member 2 (odd-paired homolog, Drosophila)	Hs.132863	AF193855.1
6	123 220184_at		Homeodomain-containing transcription factor	Hs.326290	NM_024865.1
7	113 215145_s_at		EST KIAA0868; similar to contactin associated protein	Hs.106552	AC005378
8	110 203872_at		actin, alpha 1, skeletal muscle	Hs.1288	NM_001100.2
9	98 206224_at		cystatin SN	Hs.123114	NM_001898.1
10	97 201755_at		MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (Hs.77171)	NM_006739.1	
11	92 220085_at		helicase, lymphoid-specific; proliferation-associated SNF2-like protein; (Hs.343745)	NM_018063.1	
12	77 206286_s_at		teratocarcinoma-derived growth factor 1	Hs.75561	NM_003212.1
13	73 206291_at		neurotensin	Hs.80962	NM_006183.2
14	56 214240_at		galanin	Hs.1907	AL556409
15	56 210560_at		gastrulation brain homeo box 2	Hs.184945	AF118452.1
16	53 231061_at		PROBABLE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 RNA-BINDING	Hs.278635	AF671581
17	52 231628_s_at		blastn hit: mouse desmin-binding fragment DesD19 (3.00E-86)	Hs.41072	AW262311
18	50 228038_at		blastn hit: sheep SOX-2 gene (SRY-like HMG-box transcription factor) (Hs.816)	AI669815	
19	48 215509_s_at		mitotic checkpoint kinase Bub1	AL137654.1	
20	47 206669_at		Glutamate Decarboxylase 1, isoform GAD25	NM_013445.1	
21	46 228782_at		Uteroglobin-related protein 1 (UGRP1) (NP_473364)	Hs.54795	BG540454
22	44 231407_s_at		kinesin family member C2-like	Hs.92679	AI636647
23	42 235845_at		SP1-like transcription factor (human homolog of Mouse SP5)	Hs.125276	AI380207
25	41 230356_at		unknown function; located on ch. 10; two related sequences on ch. 11	Hs.290255	AW014743
24	41 205268_s_at		adducin 2 (beta)	Hs.247423	NM_017488.1
27	41 220668_s_at		DNA (cytosine-5-)-methyltransferase 3 beta	Hs.251673	NM_006892.1
26	41 230916_at		Nodal	Hs.65853	AI050866
29	39 237275_at		ESTs, Moderately similar to S30392 phospholipase A2	<u>Hs.351262</u>	AI950472
28	39 207197_at		Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila)	Hs.111227	NM_003413.1
31	38 204126_s_at		CDC45-like protein	NM_003504.1	
30	38 242128_at		Homolog of Drosophila Orthodenticle 2 homeobox transcription factor	Hs.30837	BE779765
32	36 206456_at		gamma-aminobutyric acid (GABA) A receptor, alpha 5	Hs.24969	NM_000810.2
33	34 202870_s_at		CDC20 cell division cycle 20 homolog (S. cerevisiae)	Hs.82906	NM_001255.1
35	34 219740_at		hypothetical protein FLJ12505	Hs.125741	NM_024749.1
34	34 209372_x_at		tubulin, beta polypeptide	Hs.336780	BF971587
36	33 205046_at		centromere protein E (312kd)	Hs.75573	NM_001813.1

Table 1(a)

37	33	204766_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 1	Hs.388	NM_002452.1
38	32	208580_x_at	H4 histone family, member E		NM_021968.1
40	32	205478_at	protein phosphatase 1, regulatory (inhibitor) subunit 1A	Hs.76780	NM_006741.1
39	32	204469_at	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	Hs.78867	NM_002851.1
41	31	227434_at	hypothetical protein DKFZp761D2324	Hs.7981	AI972623
43	29	203976_s_at	chromatin assembly factor 1, subunit A (p150)	Hs.79018	NM_005483.1
42	29	212873_at	minor histocompatibility antigen HA-1	Hs.196914	BE349017
44	28	211603_s_at	Ad E1A enhancer-binding protein (ETS-domain transcription factor)		U35622.2
45	28	219170_at	fibronectin type 3 and SPRY domain-containing protein	Hs.28144	NM_024333.1
46	28	221520_s_at	hypothetical protein FLJ10468	Hs.48855	BC001651.1
47	28	209581_at	similar to rat HREV107	Hs.37189	BC001387.1
48	27	224753_at	no identification; protein product of unknown function	Hs.23044	BE614410
49	27	203129_s_at	kinesin family member 5C	Hs.6641	BF059313
52	26	241530_at	human homolog of Aspergillus sudD (suppressor of bimD6, mitotic block)	Hs.105168	AA814371
50	26	204775_at	chromatin assembly factor 1, subunit B (p60)	Hs.75238	NM_005441.1
53	26	219823_at	hypothetical protein FLJ12457	<u>Hs.86154</u>	<u>NM_024674.1</u>
51	26	221805_at	neurofilament, light polypeptide (68kD)	Hs.211584	NM_006158.1
55	25	201430_s_at	dihydropyrimidinase-like 3	Hs.74566	W72516
57	25	210457_x_at	high-mobility group (nonhistone chromosomal) protein isoforms I and Y	Hs.139800	AF176039.1
56	25	219942_at	myosin light chain 2a	Hs.75636	NM_021223.1
58	25	217728_at	S100 calcium binding protein A6 (calcyclin)	Hs.275243	NM_014624.2
54	25	205547_s_at	transgelin	Hs.75777	NM_003186.2
59	24	230195_at	no identification	Hs.152129	BF672169
62	23	209807_s_at	nuclear factor I/X (CCAAT-binding transcription factor)	Hs.35841	U18759.1
60	23	229661_at	similar to SALL1 (sal (Drosophila))-like	<u>Hs.189095</u>	<u>NM_020436.1</u>
61	23	205691_at	synaptogyrin 3	Hs.6467	NM_004209.2
64	22	204560_at	FK506-binding protein 5		NM_004117.1
63	22	204696_s_at	cell division cycle 25A	Hs.1634	NM_001789.1
65	22	205347_s_at	thymosin, beta, identified in neuroblastoma cells	Hs.56145	NM_021992.1
67	21	221051_s_at	muscle-specific beta 1 integrin binding protein	Hs.135458	NM_014446.1
66	21	206893_at	sal-like 1 (Drosophila)	Hs.123094	NM_002968.1

Table 1(b)

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